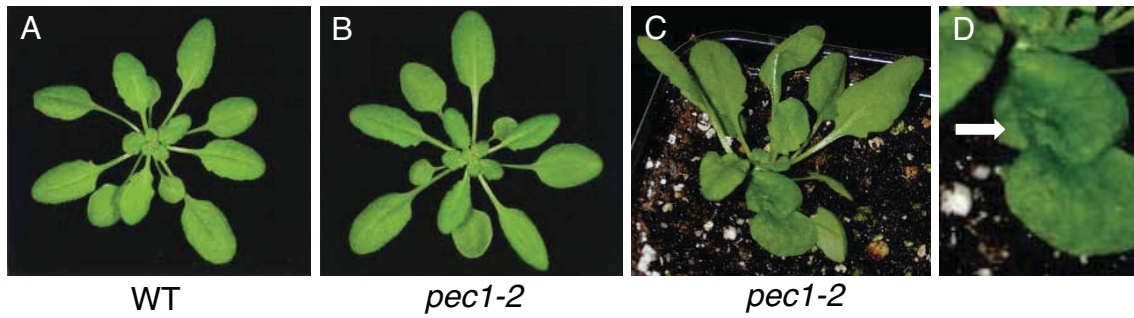


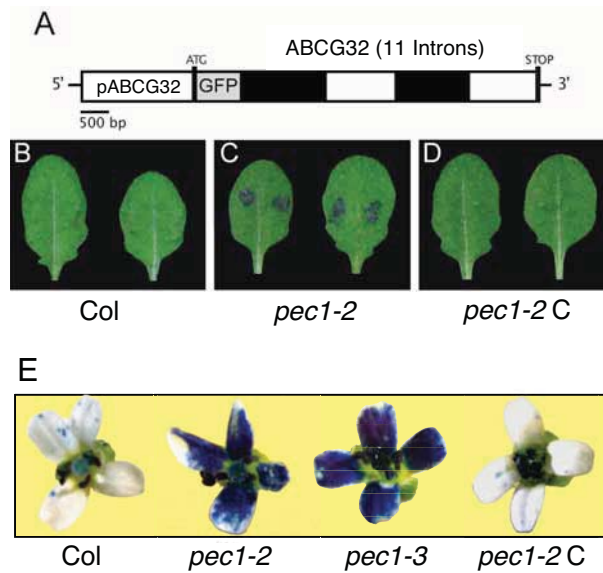
Supplemental Figure 1

Calcofluor-white staining of different genotypes. Calcofluor white-stained organs of Col-0 (A, C, E) and *pec1-2* (B, D, F) viewed under UV-light. Col-0 pictures are shown with the corresponding pictures in bright field microscopy as insert. Young seedlings (A, B), leaves (C, D), and the tip of a flowering inflorescence (E, F). Complementation analysis (G). Calcofluor stained leaves of *pec1-1* (left), *pec1-3* (middle) and an F1 plant of the cross between *pec1-1* and *pec1-3* showing that *pec1-3* cannot complement the *pec1-1* phenotype.



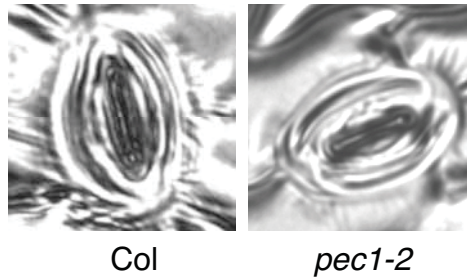
Supplemental Figure 2

Morphology of the rosette of different genotypes. (A) WT, (B-D) *pec1-2*. The *pec1* mutant alleles have mainly no visual growth phenotype (B) and only occasionally epinastic leaves and organ fusions, for example between leaves and petioles (C). (D) Enlargement of indicated area in (C). Arrow indicates zone of organ fusion.



Supplemental Figure 3

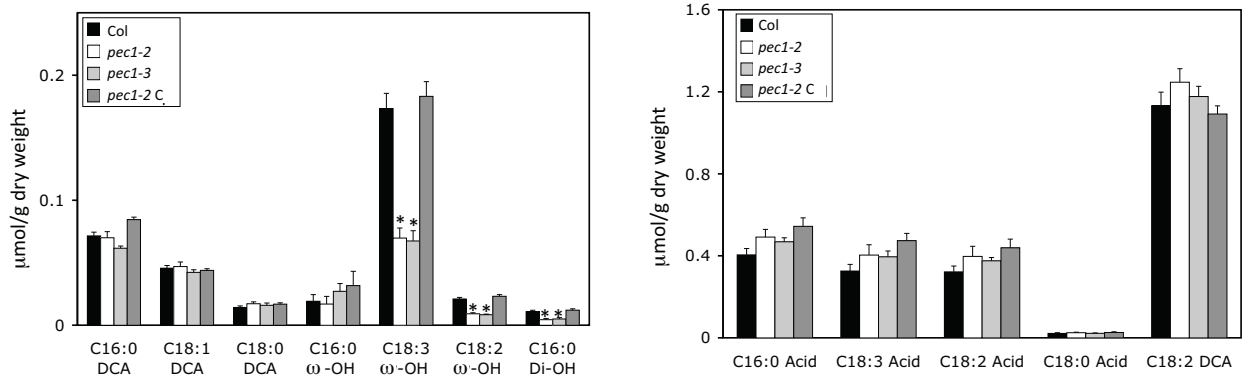
Generation of *pec1-2* lines expressing a functional GFP-ABCG32 fusion. (A) Schematic diagram of construct pABCG32:GFP-ABCG32. (B-D) TB staining of leaves from Col-0 (B), *pec1-2* (C) and a representative transgenic *pec1-2* line carrying pABCG32:GFP-ABCG32 (*pec1-2 C*). (E) TB staining of flowers from Col, *pec1-2*, *pec1-3* and *pec1-2 C*.



Supplemental Figure 4

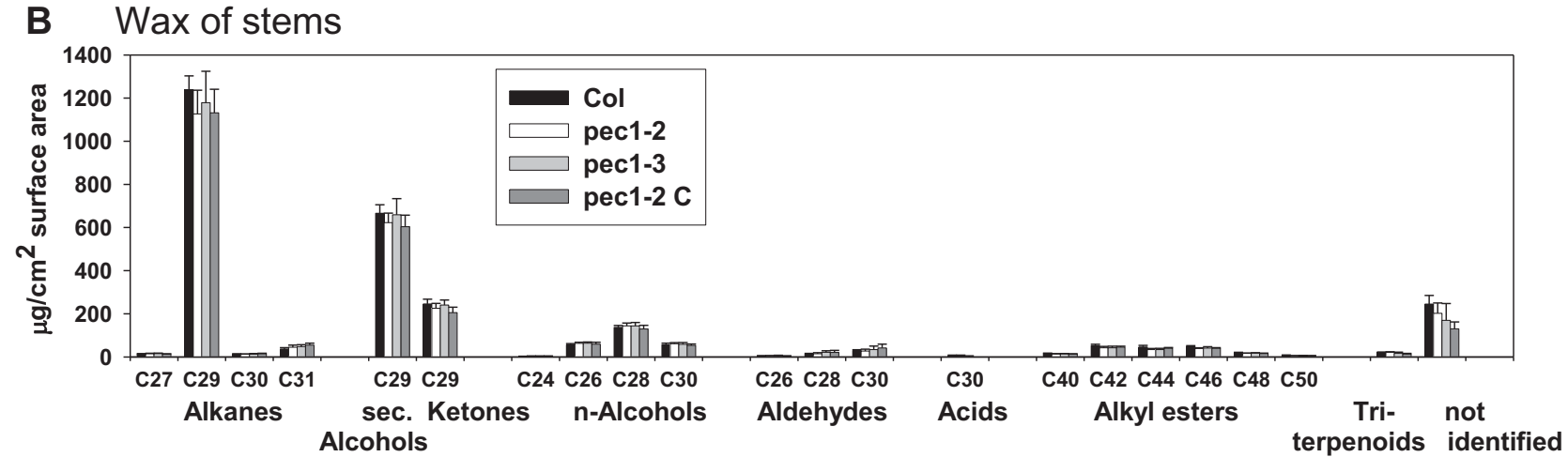
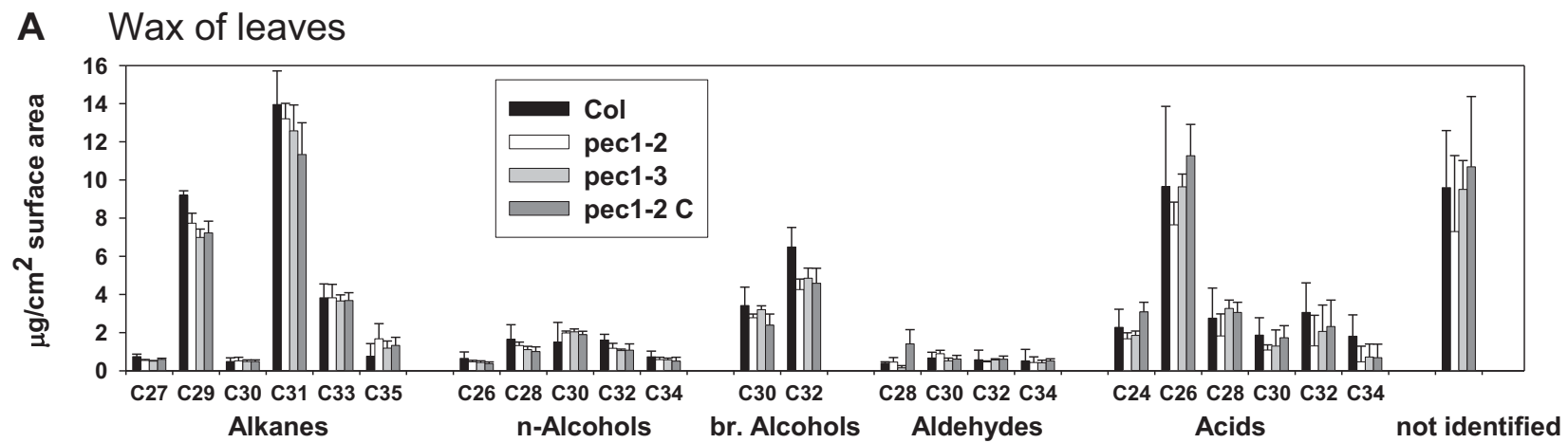
Stomata closure under drought conditions of different genotypes. The aperture of stomata of leaves from 5 to 6 weeks-old rosettes that are cut at their hypocotyls were observed. 2 hours after excision, expanded rosette leaves were pressed against fast drying nail polish (Manhattan) that had been applied to a microscopic slide. Pictures of the imprints were taken with a digital camera (Leica, DC200) on a Diaplan microscope (500X, Leitz). Col (left), *pec1-2* (right).

Residue-bound lipids of stems



Supplemental Figure 5

Biochemical analyses of residue-bound lipids of different genotypes. Polyester monomers of stems (n=5-6; +/-SE; the experiment was repeated twice with similar results). DCA, dicarboxylic acid, ω-HA, omega-hydroxy fatty acid, DHP, dihydroxypalmitate. Reductions that are significant with $P < 0.01$ are indicated by an asteriks. *pec1-2 C*, *pec1-2* expressing GFP-ABCG32.



Supplemental Figure 6

Biochemical analyses of waxes of different genotypes. (A) Leaves and (B) stems ($n=6, \pm$ SD). Wax analysis was performed on fully expanded rosette leaves of 6-weeks-old plants and on 10 cm high inflorescent stems.

Basta [nl/ml]	Col	<i>pec1-2</i>	<i>lacs2-3</i>
10	+++++	++++	+++
20	+++++	+++	+++
30	++++	+++	++
40	+++	++	+
50	+++	+	+/-
60	+++	+	+/-

Supplemental Table 1

Herbicide resistance of different genotypes. The sensitivity to BASTA® of *pec1-2* and *lacs2-3* in comparison to wt Col-0. +++++: fully green, ++++: chlorotic tips or spots, +++: whole leaves chlorotic, some dying, ++: all expanded leaves died, but vigorous regrowth, +: poor or late regrowth, +/- death or regrowth after 10 days only. Data for *lacs2* have been published previously but are included here again for direct comparison of the mutants (Bessire et al., 2007).

Primers used in this study.

attB-pABCG32-1 F	5'-GGGGACAAGTTTGTACAAAAAAGCAGGCT <u>CGGTTCCGATCGGTAGTTAT</u> -3'
attB-pABCG32-1 R	5'-GGGGACCACTTTGTACAAGAAAGCTGGGTC <u>GTTCTCCGCCGAGTTCCA</u> -3'
attB-2-ABCG32 F	5'-GGGGACAAGTTTGTACAAAAAAGCAGGCT <u>TCATGTGGAAGTCGGCGGAGAAC</u> -3'
attB-ABCG32+S R	5'-GGGGACCACTTTGTACAAGAAAGCTGGGTC <u>CTAATCAATCCATCATCTTCTCTG</u> -3'
ABCG32-qPCR F	5'- <u>GTTGTCGCCTTTTGCGTCTTCT</u> -3'
ABCG32-qPCR R	5'- <u>ATAGGCAGTCCCCTGCCCTTCTT</u> -3'
pABCG32+HindIII F	5'-ATAAGCTT <u>AGAAAGGTCTCGGGAGGAAAC</u> -3'
pABCG32+KpnI R	5'-TTAGGTACCA <u>AATCTCCGCGGCGGCGCAACAGAA</u> -3'
ABCG32-1-SP6	5'-CTCGAGTTTAGGTGACACTATAGAACTGGAG <u>GGTGTTGGATTCAAATATGATATGC</u> -3'
ABCG32-1-T7	5'-CTCGAGTAATACGACTCACTATAGGGAG <u>CTCGTCTAACTCTTCTCTGGATACAAC</u> -3'
ABCG32-2-SP6	5'-CTCGAGTTTAGGTGACACTATAGAACTGGAGC <u>CACAGGGCGAACCATTGTCTGC</u> -3'
ABCG32-2-T7	5'-CTCGAGTAATACGACTCACTATAGGGAG <u>GGCGAATGCAAAACACAAGGGAG</u> -3'
ABCG11-qPCR F	5'- <u>ATGGTCTTACCCAGTCTCCTTCTCT</u> -3'
ABCG11-qPCR R	5'- <u>TATTGCAGGCCTAGTGAAATATGGT</u> -3'
ABCG13-qPCR F	5'- <u>AGATGATTGGGGTGGAGTATGATT</u> -3'
ABCG13-qPCR R	5'- <u>CCTTTTCTGGATATGGCTCAGAGT</u> -3'

Underlined sequences are gene-specific.